SEQUENCE LISTING

<110> KISHIMOTO, Tadamitsu
      NAGASAWA, Takashi
      TACHIBANA, Kazunobu
      CHUGAI SEIYAKU KABUSIKI KAISHA

<120> Vascularization Inhibitors

<130> 46124-5042-US

<140> US 09/646,785
<141> 2001-02-16

<150> PCT/JP99/01448
<151> 1999-03-23

<150> JP10/95448
<151> 1998-03-24

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                 35   40   45
Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
                 50   55   60
Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys
                 65   70   75
Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr
                 80   85   90
Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly
                 95   100   105
Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu
                110   115   120
Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr
                125   130   135
Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu
                140   145   150
Leu Ala Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu
                155   160   165
Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn Val Ser Glu Ala
                170   175   180
Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp
                185   190   195
Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
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Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys
              215                 220                 225
Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
              230                 235                 240
Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr
              245                 250                 255
Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile
              260                 265                 270
Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser
              275                 280                 285
Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
              290                 295                 300
Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His
              305                 310                 315
Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser
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tcc atc atc ttc tta act ggc att gtg ggc aat gga ttg gtc atc 180
ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag 225
tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg 270
ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg 315
aac ttc cta tgc aag gca gtc cat gtc atc tac aca gtc aac ctc 360
tac agc agt gtc ctc atc ctg gcc ttc atc agt ctg gac cgc tac 405
ctg gcc atc gtc cac gcc acc aac agt cag agg cca agg aag ctg 450
ttg ctg aaa aag gtg gtc tat gtt ggc gtc tgg atc cct gcc ctc 495
ctg ctg act att ccc gac ttc atc ttt gcc aac gtc agt gag gca 540
gat gac aga tat atc tgt gac cgc ttc tac ccc aat gac ttg tgg 585
gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
cct ggt att gtc atc ctg tcc tgc tat tgc att atc atc tcc aag 675
ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc 720
aca gtc atc ctc atc ctg gct ttc ttc gcc tgt tgg ctg cct tac 765
tac att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc 810
aag caa ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc 855
atc acc gag gcc cta gct ttc ttc cac tgt tgt ctg aac ccc atc 900
ctc tat gct ttc ctt gga gcc aaa ttt aaa acc tct gcc cag cac 945
gca ctc acc tct gtg agc aga ggg tcc agc ctc aag atc ctc tcc 990
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tct tca agt ttt cac tcc agc taa cacagatgta aaagactttt ttttat 1085
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2

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               35                  40                      45
Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu
               50                  55                      60
Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr
               65                  70                      75
Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val
               80                  85                      90
Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp Trp Tyr
               95                 100                     105
Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val
              110                 115                     120
Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
              125                 130                     135
Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg
              140                 145                     150
Lys Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro
              155                 160                     165
Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser
              170                 175                     180
Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg
              185                 190                     195
Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln His
              200                 205                     210
Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys
              215                 220                     225
Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
              230                 235                     240
Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
              245                 250                     255
Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser
              260                 265                     270
Phe Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser
              275                 280                     285
Ile Val His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe
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4

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               20                  25                     30
Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys
               35                  40                     45
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
               50                  55                     60
Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
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Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
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<213> Mus

<220>
<221> CDS
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cgccgctccc ctccagctcg cctgcgcctc tcactctccg tcagccgcat tgcccgctcg 420
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ctc tgc ctc agc gac ggg aag ccc gtc agc ctg agc tac aga tgc 563
cca tgc cga ttc ttc gaa agc cat gtt gcc aga gcc aac gtc aag 608
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gcc cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aag 698
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                 20                  25                  30
Pro Cys Arg Phe Phe Glu Ser His Ile Ala Arg Ala Asn Val Lys
                 35                  40                  45
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
                 50                  55                  60
Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
                 65                  70                  75
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
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<212> DNA
<213> Mus

<220>
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<222> (82)...(351)

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ctc tgc atc agt gac ggt aaa cca gtc agc ctg agc tac cga tgc 171
ccc tgc cgg ttc ttc gag agc cac atc gcc aga gcc aac gtc aag 216
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tta aag tgg atc caa gag tac ctg gag aaa gct tta aac aag taa 351
gcacaacagc ccaaaggact ttccagtaga cccccgagga aggctgacat ccgtgggaga 411
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<220>
<223> added peptide

<400> 9
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<210>10
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> added peptide

<400> 10
Arg Leu Lys Met


<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence
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<220>
<223> primer

<400> 12
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